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	Filing Date		2003-07-09	
	First Named Inventor	MARANAS, COSTAS D.		
	Art Unit	1631		
	Examiner Name	SKOWRONEK, KARLHEINZ R.		
	Attorney Docket Number	P06367US03 (2 OF 2)		

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1	Moore et al., "Modeling DNA Mutation and Recombination for Directed Evolution Experiments" J. Theor. Biol. 205 (3):483-503 (2000).	<input type="checkbox"/>
2	Moore et al., "Predicting crossover generation in DNA shuffling," Proc. Natl. Acad. Sci. USA 98(6):3226-3231 (2001).	<input type="checkbox"/>
3	Mushegian et al., "A minimal gene set for cellular life derived by comparison of complete bacterial genomes," Proc. Natl. Acad. Sci. USA 93(19):10268-10273 (1996).	<input type="checkbox"/>
4	Nakamura and Whited, "Metabolic engineering for the microbial production of 1,3-propanediol," Curr. Opin. Biotechnol. 14(5):454-459 (2003).	<input type="checkbox"/>
5	Oh et al., "Gene expression profiling by DNA microarrays and metabolic fluxes in Escherichia coli," Biotechnol. Prog. 16(2):278-286 (2000).	<input type="checkbox"/>
6	Overbeek et al., "WIT: integrated system for high-throughput genome sequence analysis and metabolic reconstruction," Nucleic Acids. Res. 28(1):123-125 (2000).	<input type="checkbox"/>
7	Palsson, "The Challenges of in Silico Biology," Nat. Biotechnol. 18(11):1147-1150 (2000).	<input type="checkbox"/>
8	PAPOUTSAKIS et al., "Equations and Calculations of Product Yields and Preferred Pathways for Butanediol and Mixed-Acid Fermentations", Biotechnology and Bioengineering 17:50-66 (1985).	<input type="checkbox"/>
9	Papoutsakis, "Equations and calculations for fermentations of butyric acid bacteria," Biotechnol. Bioeng. 26(2):174-187 (1984).	<input type="checkbox"/>
10	Pennisi, "Laboratory Workhorse Decoded," Science 277:1432-1434 (1997).	<input type="checkbox"/>
11	Pharkya et al., "Exploring the overproduction of amino acids using the bilevel optimization framework OptKnock," Biotechnol. Bioeng. 84(7):887-899 (2003).	<input type="checkbox"/>

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12	Pharka, et al., "OptStrain: A computational framework for redesign of microbial production systems", Genome Res. 14:2367-2376 (2004).	<input type="checkbox"/>
13	Pramanik et al., "Stoichiometric Model of Escherichia coli Metabolism: Incorporation of Growth-Rate Dependent Biomass Composition and Mechanistic Energy Requirements," Biotechnol. Bioeng. 56(4):398-421 (1997).	<input type="checkbox"/>
14	Quackenbush et al., "The TIGR Gene Indices: analysis of gene transcript sequences in highly sampled eukaryotic species," Nucleic Acids Res. 29:159-165 (2001).	<input type="checkbox"/>
15	Reed et al., "An expanded genome-scale model of Escherichia coli K-12 (JUR904 GSM/GPR)," Genome Biol. 4(9):R54 (2003).	<input type="checkbox"/>
16	Richmond et al., "Genome-wide expression profiling in Escherichia coli K-12," Nucl. Acids Res. 27(19):3821-3835 (1999).	<input type="checkbox"/>
17	SantaLucia Jr., "A unified view of polymer, dumbbell, and oligonucleotide DNA nearest-neighbor thermodynamics," Proc. Natl. Acad. Sci. USA, 95(4):1460-1465 (1998).	<input type="checkbox"/>
18	Savageau, "Biochemical Systems Analysis," J. Theor. Biol. 25:365-369 (1969).	<input type="checkbox"/>
19	Schilling et al., "The Underlying Pathway Structure of Biochemical Reaction Networks," Proc. Natl. Acad. Sci. USA, 95 (8):4193-4198 (1998).	<input type="checkbox"/>
20	Schilling, et al., "Combining pathway analysis with flux balance analysis for the comprehensive study of metabolic systems," Biotechnol. Bioeng. 71(4):286-306 (2000).	<input type="checkbox"/>
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22	Segre et al., "From annotated genomes to metabolic flux models and kinetic parameter fitting," Omics, 7(3):301-316 (2003).	<input type="checkbox"/>

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23	Selkov, et al., "MPW: the Metabolic Pathways Database," Nucl Acids Res, 26(1):43-45 (1998).	<input type="checkbox"/>
24	Sun, "Modeling DNA Shuffling," Ann. Conf. Res. Comp. Mol. Biol. Proc. Second. Ann. Intl Conf. Comp. Mol. Biol. p. 251-257 (1998).	<input type="checkbox"/>
25	Supplemental European Search Report, The Penn State Research Foundation, EP 04 78 2168 dated 7-1-2009, 2 pages	<input type="checkbox"/>
26	Supplemental European Search Report, The Penn State Research Foundation, EP 0478 2168 Dated 7-8-2009.	<input type="checkbox"/>
27	TIGR-Web site. TIGR microbial database http://www.tigr.org (2009) (NOT AVAILABLE)	<input type="checkbox"/>
28	Tomita, et al., "E-CELL: software environment for whole-cell simulation," Bioinformatics 15(1):72-84 (1999).	<input type="checkbox"/>
29	Tomita, "The E-Cell Project: Towards Integrative Simulation of cellular Processes," New Gen. Comput. 18:1-12 (2000).	<input type="checkbox"/>
30	Torres et al., "An Indirect Optimization Method for Biochemical Systems: Description of Method and Application to the Maximization of the Rate of Ethanol, Glycerol, and Carbohydrate Production in <i>Saccharomyces cerevisiae</i> ," Biotechnol. Bioeng. 55(5):758-772 (1997).	<input type="checkbox"/>
31	Valdes et al., "Metabolic reconstruction of sulfur assimilation in the extremophile <i>Acidithiobacillus ferrooxidans</i> based on genome analysis," BMC Genomics 4:51 (2003).	<input type="checkbox"/>
32	VALLINO et al., "Metabolic flux distributions in <i>Corynebacterium glutamicum</i> during growth and lysine overproduction," Biotechnol. Bioeng. 41:633-646 (1993).	<input type="checkbox"/>
33	VARMA et al., "Metabolic Capabilities of <i>Escherichia coli</i> : I. Synthesis of Biosynthetic Precursors and Cofactors", J. theor. Biol. 165:477-502 (1993).	<input type="checkbox"/>

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34	VARMA et al., "Stoichiometric flux balance models quantitatively predict growth and metabolic by-product secretion in wild-type <i>Escherichia coli</i> W3110," <i>Appl. Environ. Microbiol.</i> 60(10):3724-3731 (Oct 1994).	<input type="checkbox"/>
35	Varner et al., "Mathematical Models of Metabolic Pathways," <i>Curr. Opin. Biotechnol.</i> 10(2):146-150 (April 1999).	<input type="checkbox"/>
36	Voit, "Optimization in Integrated Biochemical Systems," <i>Biotechnol. Bioeng.</i> 40(5):572-582 (1992).	<input type="checkbox"/>
37	Wang, et al., "Cadmium removal by a new strain <i>Pseudomonas aeruginosa</i> in aerobic culture," <i>App. Environ. Microbiol.</i> 63:4075-4078 (1997).	<input type="checkbox"/>
38	Xie et al., "Energy metabolism and ATP balance in animal cell cultivation using a stoichiometrically based reaction network," <i>Biotechnol. Bioeng.</i> 52(5):591-601 (1996).	<input type="checkbox"/>
39	Xie et al., "Integrated approaches to the design of media and feeding strategies for fed-batch cultures of animal cells," <i>Trends Biotechnol.</i> 15(3):109-113 (1997).	<input type="checkbox"/>
40	Xie et al., "Material Balance Studies on Animal Cell Metabolism Using Stoichiometrically Based Reaction Network," <i>Biotechnol. Bioeng.</i> 52:579-590 (1996).	<input type="checkbox"/>
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43	URL unix.mcs.anl.gov/otc/Guide/faq/linear-programming-faq.html , "Linear Programming Frequently asked questions," Optimization Technology Center of Northwestern University and Argonne National Laboratory (As Printed December 1, 2001).	<input type="checkbox"/>
44	URL: www.che.udel.edu/edwardsgroup/LAB/NBT_ExpPhPP/FBAPrimer/FBAC "Appendix 1: Flux balance analysis primer," (As printed 1/4/02)	<input type="checkbox"/>

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45	URL http://www.ilog.com/products/cplex/ accessed via the GAMS (Brooke, et al., (1998).	<input type="checkbox"/>
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